

SEQUENCE LISTING

<110> Bayer AG, BHC

<120> Diagnostics and Therapeutics for Diseases Associated with Arginyl Aminopeptidase RNPEP (RNPEP)

<130> Le A 36 899

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 2400

<212> DNA

<213> Homo sapiens

<400> 1

cacgaggcca	tggcgagcgg	cgagcattcc	ccggcagcg	cgccggccgg	cgccgcgtgc	60
actccgcgca	ggctgcggcc	gctgcactcc	gcgcaggctg	tggacgtggc	ctcgccctcc	120
aacttccggg	ccttgagct	gctgcacttg	cacctggacc	tgcgggctga	gttcgggcct	180
ccagggcccg	gcmcaggag	ccgggggctg	agcggcaccg	cggctctgga	cctgcgcgtgc	240
ctggagcccg	agggcgcgc	cgagctgcgg	ctggactcgc	accctgcct	ggaggtgacg	300
gcggccgcgc	tgcggcggga	gcggcccgcc	tggaggagc	cgcctgcgg	gcggcgtgacg	360
ttctacacgc	agcccttctc	gcactatggc	caggccctgt	gcgtgtccctt	ccgcagcccc	420
tgccgcgcgc	ccgagcgcct	ccaggtgctg	ctcacctacc	gcgtcgggga	gggaccgg	480
ttttgctggg	tggctcccg	gcagacagca	ggaaagaaga	agcccttcgt	gtacacccag	540
ggccaggctg	tcctaaaccg	ggccttccttc	ccttgcttcg	acacgcctgc	tgttaatac	600
aagtattcag	ctcttattga	ggtcccagat	ggcttcacag	ctgtgatgag	tgcaagacct	660
ggggagaaga	gaggtccaaa	taagttcttc	ttccagatgt	gtcagcccat	ccccccttat	720
ctgatagctt	tggccatcg	agatctggtt	tggctgaag	ttggacccag	gagccgggtg	780
tgggctgagc	cctgcctgat	tgtgctgcc	aaggagtaca	acgggggtgat	agaagaattt	840
ttggcaacag	gagagaagct	ttttggacct	tatgtttggg	gaaggttatga	cttgctttc	900
atgccaccgt	cctttccatt	tggaggaatg	gagaaccctt	gtctgacctt	tgtcaccccc	960
tgcctgctag	ctggggaccg	ctccctggca	gatgtcatca	tccatgagat	ctcccacagt	1020
tggtttggga	acctggtcac	caacgccaac	tggggtaat	tctggctcaa	tgaaggttc	1080
accatgtacg	cccagaggag	gatctccacc	atcctctttg	gcgcgtgcgt	cacctgcttg	1140
gaggctgcaa	cgggccgggc	tctgctgcgt	caacacatgg	acatcaactgg	agagaaaaac	1200
ccactcaaca	agctccgcgt	gaagattgaa	ccaggcggtt	accggacga	cacctataat	1260
gagacccct	acgagaaaagg	tttctgcttt	gtctcataacc	tggcccaactt	ggtgggtgat	1320
caggatcagt	ttgacagttt	tctcaaggcc	tatgtgcatg	aattcaaatt	ccgaagcatac	1380
ttagccgatg	actttctgga	cttctacttg	gaatattcc	ctgagcttaa	aaaaaagaga	1440

gtggatatca ttccagggtt tgagtttcatcgatggctga ataccccccgg ctggcccccgg 1500
 tacctccctg atctctcccc tggggactca ctcatgaagc ctgctgaaga gctagccaa 1560
 ctgtggcag ccgaggagct ggacatgaag gccattgaag ccgtggccat ctctccctgg 1620
 aagacctacc agctggtcta cttcctggat aagatccctc agaaaatcccc tctccctct 1680
 gggaatgtga aaaaacttgg agacacatac ccaagtatct caaatgcccgg gaatgcagag 1740
 ctccggctgc gatggggcca aatcgctt aagaacgacc accaggaaga ttctggaaa 1800
 gtgaaggagt tcctgcataa ccaggggaag cagaagtata cacttccgct gtaccacgca 1860
 atgatgggtg gcagtggagt gccccagacc ctcgccaagg agacttttgc atccaccggcc 1920
 tcccgctcc acagcaatgt tgtcaactat gtccagcaga tcgtggcacc caagggcagt 1980
 tagaggctcg tgtgcattggc ccctgcctct tcaggctctc caggcttca gaataattgt 2040
 ttgttcccaa attcctgttc cctgatcaac ttcttgaggt ttatatcccc tcaggataat 2100
 ctattctcta gcttaggtat ctgtgactct tgggcctctg ctctggggaa aacttacttc 2160
 tctatagccc actgagcccc gagacagaga acctgcccac agctctcccc gctacaggct 2220
 gcaggcacgc agggcagcgg gtatttcct cccacctaag tctctgggaa gaagtggaga 2280
 ggactgtatgc tctttttt tctctttctg tccttttct tgctgattta tgcaaaggc 2340
 tggcattctg atgctttca ggttaatcc ttattttaat aaagtttca agcaaaaaaa 2400

<210> 2
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys Leu Thr
 1 5 10 15
 Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala Asp Val
 20 25 30
 Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val Thr Asn
 35 40 45
 Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met Tyr Ala
 50 55 60
 Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr Cys Leu
 65 70 75 80
 Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp Ile Thr
 85 90 95
 Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu Pro Gly
 100 105 110
 Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys Gly Phe
 115 120 125
 Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp Gln Phe
 130 135 140
 Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg Ser Ile
 145 150 155 160

Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro Glu Leu
165 170 175
Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp Arg Trp
180 185 190
Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser Pro Gly
195 200 205
Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp Ala Ala
210 215 220
Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser Pro Trp
225 230 235 240
Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln Lys Ser
245 250 255
Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr Pro Ser
260 265 270
Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly Gln Ile
275 280 285
Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys Glu Phe
290 295 300
Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr His Ala
305 310 315 320
Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu Thr Phe
325 330 335
Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr Val Gln
340 345 350
Gln Ile Val Ala Pro Lys Gly Ser
355 360

<210> 3

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> forward primer

<400> 3

gaagattgaa ccaggcgttg a

21

<210> 4

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> reverse primer

<400> 4

ggtatgagac aaagcagaaa ccttt

25

<210> 5

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> probe

<400> 5

ccggacgaca cctataatga gacccctac

30